

Query= SEQ ID NO:43
 (1650 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC018552.5.95189.106311	569	e-159
AC018552.5.17437.94328	297	1e-77

>AC018552.5.95189.106311
 Length = 11123

Score = 569 bits (287), Expect = e-159
 Identities = 287/287 (100%)
 Strand = Plus / Plus

Query: 1257 atgctggttccgtgaagggacaacccatgtacgccctctatatcacccgtccacggctactt 1316
 |||
 Sbjct: 5423 atgctggttccgtgaagggacaacccatgtacgccctctatatcacccgtccacggctactt 5482

Query: 1317 cctcatcaccttccctctttggcatggtggtcctggccctggtggtctggaagatcttcac 1376
 |||
 Sbjct: 5483 cctcatcaccttccctctttggcatggtggtcctggccctggtggtctggaagatcttcac 5542

Query: 1377 cctgtcccgtgctacagcgggtcaaggagcgggggaagaaccggaagaaggtgctcacccct 1436
 |||
 Sbjct: 5543 cctgtcccgtgctacagcgggtcaaggagcgggggaagaaccggaagaaggtgctcacccct 5602

Query: 1437 gctgggcctctcgagcctggtgggtgtgacatgggggttgccatcttcaccccggtggg 1496
 |||
 Sbjct: 5603 gctgggcctctcgagcctggtgggtgtgacatgggggttgccatcttcaccccggtggg 5662

Query: 1497 cctctccaccgtctacatctttgcacttttcaactccttgcaaggtg 1543
 |||
 Sbjct: 5663 cctctccaccgtctacatctttgcacttttcaactccttgcaaggtg 5709

Score = 563 bits (284), Expect = e-157
 Identities = 284/284 (100%)
 Strand = Plus / Plus

Query: 880 aggcctttccgggagaggttcaagtcagaagatgccccaaagatccacgtggccctgggt 939
 |||
 Sbjct: 3710 aggcctttccgggagaggttcaagtcagaagatgccccaaagatccacgtggccctgggt 3769

Query: 940 ggcagcctgttccctcctgaatctggccttcttgggtcaatgtggggagtgggtcaaagggg 999
 |||
 Sbjct: 3770 ggcagcctgttccctcctgaatctggccttcttgggtcaatgtggggagtgggtcaaagggg 3829

Query: 1000 tctgatgctgcctgctgggcccgggggctgtcttccactacttcctgctctgtgccttc 1059
|||||
Sbjct: 3830 tctgatgctgcctgctgggcccgggggctgtcttccactacttcctgctctgtgccttc 3889

Query: 1060 acctggatgggccttgaagccttccacctctacctgctcgctgtcagggctttcaacacc 1119
|||||
Sbjct: 3890 acctggatgggccttgaagccttccacctctacctgctcgctgtcagggctttcaacacc 3949

Query: 1120 tacttcgggcactacttcctgaagctgagcctggtgggctgggg 1163
|||||
Sbjct: 3950 tacttcgggcactacttcctgaagctgagcctggtgggctgggg 3993

Score = 228 bits (115), Expect = 9e-57
Identities = 115/115 (100%)
Strand = Plus / Plus

Query: 768 gagaccaccttggaccagtccacggtgcatacctcacacgcatctcccagggcgggctg 827
|||||
Sbjct: 284 gagaccaccttggaccagtccacggtgcatacctcacacgcatctcccagggcgggctg 343

Query: 828 tggggctctccatgatcttcctggccttcaccattattctttatgcctttctgagg 882
|||||
Sbjct: 344 tggggctctccatgatcttcctggccttcaccattattctttatgcctttctgagg 398

Score = 204 bits (103), Expect = 1e-49
Identities = 103/103 (100%)
Strand = Plus / Plus

Query: 1539 aggtgtcttcatctgctgctggttcaccatcctttacctcccaagtcagagcaccacagt 1598
|||||
Sbjct: 8131 aggtgtcttcatctgctgctggttcaccatcctttacctcccaagtcagagcaccacagt 8190

Query: 1599 ctctcctctactgcaagattggaccaggccactccgcatct 1641
|||||
Sbjct: 8191 ctctcctctactgcaagattggaccaggccactccgcatct 8233

Score = 204 bits (103), Expect = 1e-49
Identities = 103/103 (100%)
Strand = Plus / Plus

Query: 666 agggaccactggagactggtcttctgagggctgctccacggaggtcagacctgaggggac 725
|||||
Sbjct: 43 agggaccactggagactggtcttctgagggctgctccacggaggtcagacctgaggggac 102

Query: 726 cgtgtgctgctgtgaccacctgacctttttcgccctgctcctg 768
|||||
Sbjct: 103 cgtgtgctgctgtgaccacctgacctttttcgccctgctcctg 145

Score = 188 bits (95), Expect = 8e-45
Identities = 95/95 (100%)
Strand = Plus / Plus

Query: 1162 ggccctgcccgcctgatgggtcatcggcactgggagtgccaacagctacggcctctacacc 1221
|||||
Sbjct: 4169 ggccctgcccgcctgatgggtcatcggcactgggagtgccaacagctacggcctctacacc 4228

Query: 1222 atccgtgatagggaacccgcacctctctggagct 1256
|||||
Sbjct: 4229 atccgtgatagggaacccgcacctctctggagct 4263

>AC018552.5.17437.94328
Length = 76892

Score = 297 bits (150), Expect = 1e-77
Identities = 150/150 (100%)
Strand = Plus / Plus

Query: 57 aggtcaggaaaagcccaccgaagggccaaagaaacacctgcctggggagcaacaacatgta 116
|||||
Sbjct: 68998 aggtcaggaaaagcccaccgaagggccaaagaaacacctgcctggggagcaacaacatgta 69057

Query: 117 cgacatcttcaacttgaatgacaaggctttgtgcttcaccaagtgcaggcagtcgggcag 176
|||||
Sbjct: 69058 cgacatcttcaacttgaatgacaaggctttgtgcttcaccaagtgcaggcagtcgggcag 69117

Query: 177 cgactcctgcaatgtggaaaacttgcagag 206
|||||
Sbjct: 69118 cgactcctgcaatgtggaaaacttgcagag 69147

Score = 297 bits (150), Expect = 1e-77
Identities = 150/150 (100%)
Strand = Plus / Plus

Query: 344 aggttccgaggcaggtgatgaaggacgaggacaagccccctgacagagtgcgacttcca 403
|||||
Sbjct: 73847 aggttccgaggcaggtgatgaaggacgaggacaagccccctgacagagtgcgacttcca 73906

Query: 404 agagcctttttcgatccctgccaggcaacaggtctgtgggtccgcttggccgctcaccattc 463
|||||
Sbjct: 73907 agagcctttttcgatccctgccaggcaacaggtctgtgggtccgcttggccgctcaccattc 73966

Query: 464 tggacattgggtccagggactctcttcaagg 493
|||||
Sbjct: 73967 tggacattgggtccagggactctcttcaagg 73996

Score = 283 bits (143), Expect = 2e-73
Identities = 143/143 (100%)
Strand = Plus / Plus

Query: 205 agatactgggctaaactacgaggcccatctgatgaaggaaggtttgacgcagaaggtgaac 264
|||||
Sbjct: 71877 agatactgggctaaactacgaggcccatctgatgaaggaaggtttgacgcagaaggtgaac 71936

Query: 265 acgcctttcctgaaggctttgggtccagaacctcagcaccaaacactgcagaagacttctat 324
|||||
Sbjct: 71937 acgcctttcctgaaggctttgggtccagaacctcagcaccaaacactgcagaagacttctat 71996

Query: 325 ttctctctggagccctctcaggt 347
|||||
Sbjct: 71997 ttctctctggagccctctcaggt 72019

Score = 272 bits (137), Expect = 7e-70
Identities = 141/142 (99%), Gaps = 1/142 (0%)
Strand = Plus / Plus

Query: 487 ttca-aggggcccccggtcggcctgggagatggcagcggtgttgacaatcgccctggt 545
|||||
Sbjct: 74849 ttcacaggggcccccggtcggcctgggagatggcagcggtgttgacaatcgccctggt 74908

Query: 546 gggtttgagtgtgggacaaatgcatgtcaccaagctgggtgagcctctggagatcgtctt 605
|||||
Sbjct: 74909 gggtttgagtgtgggacaaatgcatgtcaccaagctgggtgagcctctggagatcgtctt 74968

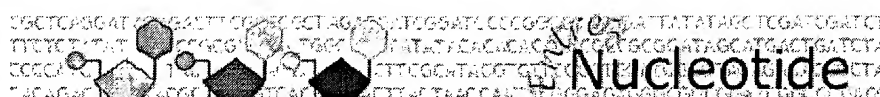
Query: 606 ctctcaccagcgaccgccccct 627
|||||
Sbjct: 74969 ctctcaccagcgaccgccccct 74990

Score = 119 bits (60), Expect = 6e-24
Identities = 60/60 (100%)
Strand = Plus / Plus

Query: 1 atggcgacgcccagggggcctggggggccctgctcctgctcctcctgctcccgacctcaggt 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 64026 atggcgacgcccagggggcctggggggccctgctcctgctcctcctgctcccgacctcaggt 64085

Score = 81.8 bits (41), Expect = 1e-12
Identities = 41/41 (100%)
Strand = Plus / Plus

Query: 628 aacatgaccctcacctgtgtattctgggatgtgactaaagg 668
||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 75495 aacatgaccctcacctgtgtattctgggatgtgactaaagg 75535



PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Boo

Search for

Limits

Preview/Index

History

Clipboard

Details

Display

Show:

Send to

☐ 1: AC018552. Homo sapiens chro...[gi:27476108]

Links

LOCUS AC018552 152156 bp DNA linear PRI 03-JAN-2003
 DEFINITION Homo sapiens chromosome 16 clone RP11-405F3, complete sequence.
 ACCESSION AC018552
 VERSION AC018552.6 GI:27476108
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 152156)
 AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
 Alamos National Laboratory.
 TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 152156)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (14-DEC-1999) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 3 (bases 1 to 152156)
 AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
 Alamos National Laboratory.
 TITLE Direct Submission
 JOURNAL Submitted (03-JAN-2003) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 COMMENT On Jan 3, 2003 this sequence version replaced gi:13786352.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center and Los Alamos
 National Laboratory
 www-shgc.stanford.edu
 Quality: Phrap Quality >=40 99.8% of Sequence;
 Estimated Total Number of Errors is 0.2.
 FEATURES Location/Qualifiers
 source 1..152156
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="RP11-405F3"
 BASE COUNT 37744 a 39980 c 38771 g 35661 t
 ORIGIN
 1 gaattccagc cacagacgtg tctgttcaag gttccacct gaccagaaa gagggcaaag
 61 caccttctcc ctggcattcc gtgcccgagc ctggtgtcct ctccgtggag gcactgctcg
 121 cccccctgg cctacctgga gggctctgtc tgtccctgg cctcactcc tccagggaa
 181 agtgtctggc tgggcccac ctcactgggc ctgagactg ctgccctgg agtcagggc
 241 attcattcat aatatcagta tttcctgggt gctgttcta ggccttgac gaaatatgcc
 301 ccagtataat cagatggtgg tggggcgagg aactgagct ggcaaaaccg cagactttgg